



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/733,288  
Source: 1FWO -  
Date Processed by STIC: 12/30/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 14733,288

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 12/30/2003

PATENT APPLICATION: US/10/733,288

TIME: 11:29:15

Input Set : A:\p24684.sql.txt

Output Set: N:\CRF4\12302003\J733288.raw

2 <110> APPLICANT: RIKEN  
 3 <120> TITLE OF INVENTION: A blood coagulation factor activating protein and an antibody thereof  
 4 <130> FILE REFERENCE: FA1128A/US  
 C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/733,288  
 C--> 5 <141> CURRENT FILING DATE: 2003-12-12  
 E--> 5 <160> NUMBER OF SEQ ID NOS: 3

4(p.2)

## ERRORED SEQUENCES

Does Not Comply  
 Corrected Dickette Needed

pr 1-3

6 <210> SEQ ID NO: 1  
 7 <211> LENGTH: 17  
 8 <212> TYPE: PRT  
 9 <213> ORGANISM: human  
 10 <220> FEATURE:  
 11 <222> LOCATION: 1  
 12 <223> OTHER INFORMATION: Unknown amino acid  
 13 <220> FEATURE:  
 14 <222> LOCATION: 2  
 15 <223> OTHER INFORMATION: Unknown amino acid  
 16 <400> SEQUENCE: 1  
 W--> 17 Xaa Xaa Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser His His  
 E--> 18 1 5 5 10 10 15 15  
 19 Asp  
 20 <210> SEQ ID NO: 2  
 21 <211> LENGTH: 18  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: human  
 24 <400> SEQUENCE: 2  
 25 Ile Val Gly Gly Arg Arg Ala Arg Pro His Ala Trp Pro Phe Met Val  
 E--> 26 1 5 5 10 10 15 15  
 27 Ser Leu  
 28 <210> SEQ ID NO: 3  
 29 <211> LENGTH: 218  
 30 <212> TYPE: PRT  
 31 <213> ORGANISM: human  
 32 <220> FEATURE:  
 33 <222> LOCATION: 218  
 34 <223> OTHER INFORMATION: Unknown amino acid  
 35 <400> SEQUENCE: 3  
 36 Ile Val Gly Gly Arg Arg Ala Arg Pro His Ala Trp Pro Phe Met Val  
 E--> 37 1 5 10 15  
 38 Ser Leu Gln Leu Arg Gly Gly Phe Phe Cys Gly Ala Thr Leu Ile Ala

misaligned nos.  
 (see item 3  
 on Error  
 summary  
 sheet)

same error

same error

## RAW SEQUENCE LISTING

DATE: 12/30/2003

PATENT APPLICATION: US/10/733,288

TIME: 11:29:15

Input Set : A:\p24684.sql.txt

Output Set: N:\CRF4\12302003\J733288.raw

```

E--> 39          20          25          30
      40 Pro Asn Phe Val Met Ser Ala Ala His Cys Val Ala Asn Val Asn Val
E--> 41          35          40          45
      42 Arg Ala Val Arg Val Val Leu Gly Ala His Asn Leu Ser Arg Arg Glu
E--> 43          50          55          60
      44 Pro Thr Arg Gln Val Phe Ala Val Gln Arg Ile Phe Glu Asn Gly Tyr
E--> 45 65          70          75          80
      46 Asp Pro Val Asn Leu Leu Asn Asp Ile Val Ile Leu Gln Leu Asn Gly
E--> 47          85          90          95
      48 Ser Ala Thr Ile Asn Ala Asn Val Gln Val Ala Gln Leu Pro Ala Gln
E--> 49          100         105         110
      50 Gly Arg Arg Leu Gly Asn Gly Val Gln Cys Leu Ala Met Gly Trp Gly
E--> 51          115         120         125
      52 Leu Leu Gly Arg Asn Arg Gly Ile Ala Ser Val Leu Gln Glu Leu Asn
E--> 53          130         135         140
      54 Val Thr Val Val Thr Ser Leu Cys Arg Arg Ser Asn Val Cys Thr Leu
E--> 55 145         150         155         160
      56 Val Arg Gly Arg Gln Ala Gly Val Cys Phe Gly Asp Ser Gly Ser Pro
E--> 57          165         170         175
      58 Leu Val Cys Asn Gly Leu Ile His Gly Ile Ala Ser Phe Val Arg Gly
E--> 59          180         185         190
      60 Gly Cys Ala Ser Gly Leu Tyr Pro Asp Ala Phe Ala Pro Val Ala Gln
E--> 61          195         200         205
W--> 62 Phe Val Asn Trp Ile Asp Ser Ile Ile Xaa
E--> 63          210         215
      65 <210> SEQ ID NO: 4
      66 <211> LENGTH: 219
      67 <212> TYPE: PRT
      68 <213> ORGANISM: human
      69 <400> SEQUENCE: 4
      70 Ile Val Gly Gly Arg Arg Ala Arg Pro His Ala Trp Pro Phe Met Val
E--> 71 1          5          10          15
      72 Ser Leu Gln Leu Arg Gly Gly His Phe Cys Gly Ala Thr Leu Ile Ala
E--> 73          20          25          30
      74 Pro Asn Phe Val Met Ser Ala Ala His Cys Val Ala Asn Val Asn Val
E--> 75          35          40          45
      76 Arg Ala Val Arg Val Val Leu Gly Ala His Asn Leu Ser Arg Arg Glu
E--> 77          50          55          60
      78 Pro Thr Arg Gln Val Phe Ala Val Gln Arg Ile Phe Glu Asn Gly Tyr
E--> 79 65          70          75          80
      80 Asp Pro Val Asn Leu Leu Asn Asp Ile Val Ile Leu Gln Leu Asn Gly
E--> 81          85          90          95
      82 Ser Ala Thr Ile Asn Ala Asn Val Gln Val Ala Gln Leu Pro Ala Gln
E--> 83          100         105         110
      84 Gly Arg Arg Leu Gly Asn Gly Val Gln Cys Leu Ala Met Gly Trp Gly
E--> 85          115         120         125
      86 Leu Leu Gly Arg Asn Arg Gly Ile Ala Ser Val Leu Gln Glu Leu Asn
E--> 87          130         135         140
      88 Val Thr Val Val Thr Ser Leu Cys Arg Arg Ser Asn Val Cys Thr Leu

```

*same**last sequence in submitted file**same**even*

DATE: 12/30/2003

TIME: 11:29:15

Input Set : A:\p24684.sql.txt

Output Set: N:\CRF4\12302003\J733288.raw

```

E--> 89 145                      150                      155                      160
      90 Val Arg Gly Arg Gln Ala Gly Val Cys Phe Gly Asp Ser Gly Ser Pro
E--> 91                      165                      170                      175
      92 Leu Val Cys Asn Gly Leu Ile His Gly Ile Ala Ser Phe Val Arg Gly
E--> 93                      180                      185                      190
      94 Gly Cys Ala Ser Gly Leu Tyr Pro Asp Ala Phe Ala Pro Val Ala Gln
E--> 95                      195                      200                      205
      96 Phe Val Asn Trp Ile Asp Ser Ile Ile Gln Arg
E--> 97                      210                      215

```

same

## VERIFICATION SUMMARY

DATE: 12/30/2003

PATENT APPLICATION: US/10/733,288

TIME: 11:29:16

Input Set : A:\p24684.sql.txt

Output Set: N:\CRF4\12302003\J733288.raw

L:5 M:270 C: Current Application Number differs, Replaced Current Application No  
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:17 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:1  
L:17 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0  
L:18 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
L:26 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
L:37 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3  
M:332 Repeated in SeqNo=3  
L:62 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3  
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:208  
L:71 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4  
M:332 Repeated in SeqNo=4  
L:5 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (3) Counted (4)